

Independent claims:

110. An isolated nucleic acid molecule comprising a nucleic acid sequence that encodes:

- (a) a polypeptide having the amino acid sequence of SEQ ID NO:2; or
- (b) a polypeptide that comprises a contiguous sequence of at least about 16 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50.

113. An isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide that comprises a contiguous sequence of at least about 16 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50.

137. An isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a P-TEFb large subunit protein, wherein said nucleic acid molecule comprises the nucleotide sequence of:

the coding sequence of a cDNA molecule present in a nucleic acid library, wherein the cDNA molecule hybridizes to a probe having the sequence of the complement of SEQ ID NO:3, SEQ ID NO:43 or SEQ ID NO:48 under conditions of high stringency.

149. An isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a P-TEFb large subunit protein that exhibits at least 90% identity to the amino acid sequence set forth in SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50, wherein said P-TEFb large subunit protein binds to a P-TEFb kinase subunit protein to form a P-TEFb enzyme complex that promotes transcription elongation.

152. An isolated nucleic acid molecule comprising:

- (a) a first nucleic acid sequence that encodes a polypeptide that comprises a contiguous sequence of at least about 16 amino acids from SEQ ID NO:2 or SEQ ID NO:6; and
- (b) a second nucleic acid sequence that encodes a polypeptide that comprises a contiguous sequence of at least about 16 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50.

Hypothetical multiply-dependent claim:

198. An isolated nucleic acid molecule of claim 110, 113, 137, 149 or 152, further comprising
.....

198. An isolated nucleic acid molecule of claim 110, 113, 137, 149 or 152, wherein said
nucleic acid molecule

Completely separate independent claim:

198. A recombinant host cell comprising an isolated nucleic acid molecule in accordance with
claim 110, claim 113, claim 137, claim 149 or claim 152.

Note that claim 198 refers to a "recombinant host cell", **NOT** "an isolated nucleic acid
molecule". Also, there is no reference to any other claim in the preamble or transitional phrase of
the claim. It is therefore, **NOT** dependent, in **any** sense, on **any** claim.

Although laborious and more difficult to read, and thus contrary to 35 U.S.C. § 112, second paragraph, claim 198 could be revised to read:

198. A recombinant host cell comprising an isolated nucleic acid molecule comprising a nucleic acid sequence that:

- (a) encodes a polypeptide having the amino acid sequence of SEQ ID NO:2; or a polypeptide that comprises a contiguous sequence of at least about 16 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50;
- (b) encodes a polypeptide that comprises a contiguous sequence of at least about 16 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50;
- (c) encodes a P-TEFb large subunit protein, wherein said nucleic acid molecule comprises the nucleotide sequence of the coding sequence of a cDNA molecule present in a nucleic acid library, wherein the cDNA molecule hybridizes to a probe having the sequence of the complement of SEQ ID NO:3, SEQ ID NO:43 or SEQ ID NO:48 under conditions of high stringency;
- (d) encodes a P-TEFb large subunit protein that exhibits at least 90% identity to the amino acid sequence set forth in SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50, wherein said P-TEFb large subunit protein binds to a P-TEFb kinase subunit protein to form a P-TEFb enzyme complex that promotes transcription elongation; or
- (e) comprises a first nucleic acid sequence that encodes a polypeptide that comprises a contiguous sequence of at least about 16 amino acids from SEQ ID NO:2 or SEQ ID NO:6; and a second nucleic acid sequence that encodes a polypeptide that comprises a contiguous sequence of at least about 16 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50.

The long format of the claim is more burdensome for the P.T.O. and the public to proof-read and interpret. Applicants are thus being financially penalized for complying with 35 U.S.C. § 112, second paragraph, and for benefiting both the P.T.O. and the public.

WILLIAMS, MORGAN & AMERSON, P.C.

7676 Hillmont, Suite 250, Houston, TX 77040
(713) 934-7000 Fax (713) 934-7011

Fax

To:	Examiner Peter Tung – U.S. Patent and Trademark Office	From:	Carolanne M. King, Reg. No. 44,914 – Assistant to Shelley P.M. Fussey
Fax:	1.703.308.0294	Phone:	713.934.4085
No. of Pages:	3	Date:	July 17, 2000
Re:	U.S. Patent Application Serial No. 08/951,188	File:	4200.000200

☐ Urgent ☐ For Review ☐ For Your File ☒ Please Reply ☐ Please Handle

* w/o coversheet

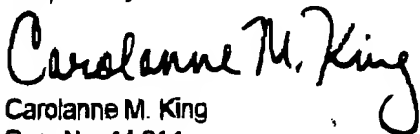
ORIGINAL: ☐ Will follow ☒ Will not follow

• **Comments:**

Examiner Tung:

Transmitted herewith are copies of the hypothetical claim materials that we have requested you to review with respect to the Request for Refund filed December 22, 1999. We would appreciate any assistance you can offer to advise the refund clerk handling our Request for Refund. Please telephone me at 713. 934.4085 after you have had an opportunity to review these materials so that we can move forward with respect to the captioned application.

Respectfully submitted


Carolanne M. King
Reg. No. 44,914

CONFIDENTIALITY NOTE

The documents accompanying this facsimile transmission contain information from the law firm of Williams, Morgan & Amerson which may be confidential and/or privileged. The information is intended to be for the use of the individual or entity named on this transmission sheet. If you are not the intended recipient, be aware that any disclosure, copying, distribution or use of the contents of this faxed information is prohibited. If you have received this facsimile in error, please notify us by telephone immediately so that we can arrange for the retrieval of the original documents at no cost to you.